SEQUENCE LISTING

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<110>  UMBI
       Bryan, Philip N.

<120>  Engineered Proteases for Affinity Purification and Processing of
       Fusion Proteins

<130>  4115-181

<140>  10/567,073
<141>  2006-02-03

<150>  US 60/493,032
<151>  2003-08-06

<150>  PCT/US04/021049
<151>  2004-06-29

<160>  8

<170>  PatentIn version 3.3

<210>  1
<211>  30
<212>  PRT
<213>  Bacillus amyloliquefaciens

<400>  1

Met Arg Gly Lys Lys Val Trp Ile Ser Leu Leu Phe Ala Leu Ala Leu
1               5                   10                  15

Ile Phe Thr Met Ala Phe Gly Ser Thr Ser Ser Ala Gln Ala
            20                  25                  30


<210>  2
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<213>  Bacillus amyloliquefaciens

<400>  2

Ala Gly Lys Ser Asn Gly Glu Lys Lys Tyr Ile Val Gly Phe Lys Gln
1               5                   10                  15

Thr Met Ser Thr Met Ser Ala Ala Lys Lys Lys Asp Val Ile Ser Glu
            20                  25                  30

Lys Gly Gly Lys Val Gln Lys Gln Phe Lys Tyr Val Asp Ala Ala Ser
        35                  40                  45

Ala Thr Leu Asn Glu Lys Ala Val Lys Glu Leu Lys Lys Asp Pro Ser
    50                  55                  60

Val Ala Tyr Val Glu Glu Asp His Val Ala His Ala Tyr
65                  70                  75
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<210> 3
<211> 275
<212> PRT
<213> Bacillus amyloliquefaciens

<400> 3

Ala Gln Ser Val Pro Tyr Gly Val Ser Gln Ile Lys Ala Pro Ala Leu
1   5   10   15

His Ser Gln Gly Tyr Thr Gly Ser Asn Val Lys Val Ala Val Ile Asp
                20   25   30

Ser Gly Ile Asp Ser Ser His Pro Asp Leu Lys Val Ala Gly Gly Ala
            35   40   45

Ser Met Val Pro Ser Glu Thr Asn Pro Phe Gln Asp Asn Asn Ser His
        50   55   60

Gly Thr His Val Ala Gly Thr Val Ala Ala Leu Asn Asn Ser Ile Gly
65   70   75   80

Val Leu Gly Val Ala Pro Ser Ala Ser Leu Tyr Ala Val Lys Val Leu
                85   90   95

Gly Ala Asp Gly Ser Gly Gln Tyr Ser Trp Ile Ile Asn Gly Ile Glu
                100   105   110

Trp Ala Ile Ala Asn Asn Met Asp Val Ile Asn Met Ser Leu Gly Gly
            115   120   125

Pro Ser Gly Ser Ala Ala Leu Lys Ala Ala Val Asp Lys Ala Val Ala
    130   135   140

Ser Gly Val Val Val Val Ala Ala Ala Gly Asn Glu Gly Thr Ser Gly
145   150   155   160

Ser Ser Ser Thr Val Gly Tyr Pro Gly Lys Tyr Pro Ser Val Ile Ala
                165   170   175

Val Gly Ala Val Asp Ser Ser Asn Gln Arg Ala Ser Phe Ser Ser Val
                180   185   190

Gly Pro Glu Leu Asp Val Met Ala Pro Gly Val Ser Ile Gln Ser Thr
            195   200   205

Leu Pro Gly Asn Lys Tyr Gly Ala Tyr Asn Gly Thr Ser Met Ala Ser
    210   215   220

```
Pro His Val Ala Gly Ala Ala Ala Leu Ile Leu Ser Lys His Pro Asn
225             230             235                 240

Trp Thr Asn Thr Gln Val Arg Ser Ser Leu Glu Asn Thr Thr Thr Lys
                245             250                 255

Leu Gly Asp Ser Phe Tyr Tyr Gly Lys Gly Leu Ile Asn Val Gln Ala
                260             265                 270

Ala Ala Gln
        275
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<210> 4
<211> 75
<212> PRT
<213> Artificial Sequence

<220>
<223> pR8 variant of SEQ ID NO: 2

<400> 4

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Ala Gly Lys Ser Asn Gly Glu Lys Lys Tyr Ile Val Gly Phe Lys Ser
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Gly Ile Lys Ser Cys Ala Lys Lys Gln Asp Val Ile Ser Glu Lys Gly
                20              25                  30

Gly Lys Leu Gln Lys Cys Phe Lys Tyr Val Asp Ala Ala Ser Ala Thr
        35              40                  45

Leu Asn Glu Lys Ala Val Lys Glu Leu Lys Lys Asp Pro Ser Val Ala
    50              55                  60

Tyr Val Glu Glu Asp Lys Val Ala Lys Ala Tyr
65              70                  75
```

<210> 5
<211> 75
<212> PRT
<213> Artificial Sequence

<220>
<223> pR8FKAM variant of SEQ ID NO: 2

<400> 5

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Ala Gly Lys Ser Asn Gly Glu Lys Lys Tyr Ile Val Gly Phe Lys Ser
1               5                   10                  15

Gly Ile Lys Ser Cys Ala Lys Lys Gln Asp Val Ile Ser Glu Lys Gly
```

```
                  20                    25                    30
```

```
Gly Lys Leu Gln Lys Cys Phe Lys Tyr Val Asp Ala Ala Ser Ala Thr
        35                    40                    45
```

```
Leu Asn Glu Lys Ala Val Lys Glu Leu Lys Lys Asp Pro Ser Val Ala
    50                    55                    60
```

```
Tyr Val Glu Glu Asp Lys Val Phe Lys Ala Met
65                    70                    75
```

```
<210>  6
<211>  75
<212>  PRT
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<400>  6
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Ala Gly Lys Ser Asn Gly Glu Lys Lys Tyr Ile Val Gly Phe Lys Ser
1                     5                    10                    15
```

```
Gly Ile Lys Ser Cys Ala Lys Lys Gln Asp Val Ile Ser Glu Lys Gly
        20                    25                    30
```

```
Gly Lys Leu Gln Lys Cys Phe Lys Tyr Val Asp Ala Ala Ser Ala Thr
        35                    40                    45
```

```
Leu Asn Glu Lys Ala Val Lys Glu Leu Lys Lys Asp Pro Ser Val Ala
    50                    55                    60
```

```
Tyr Val Glu Glu Asp Lys Val Phe Arg Ala Met
65                    70                    75
```

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<210>  7
<211>  9
<212>  PRT
<213>  Artificial Sequence
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<220>
<223>  C-terminal portion of prodomain
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<221>  VARIANT
<222>  (6)..(6)
<223>  Xaa is Phe or Tyr
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<220>
<221>  VARIANT
<222>  (9)..(9)
<223>  Xaa is Met, Lys or Tyr
```

<400> 7

Glu Glu Asp Lys Leu Xaa Gln Ser Xaa
1   5

<210> 8
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Residues 16-21 of SEQ ID NO: 2

<400> 8

Gln Thr Met Ser Thr Met
1   5